

002201" 50/86960

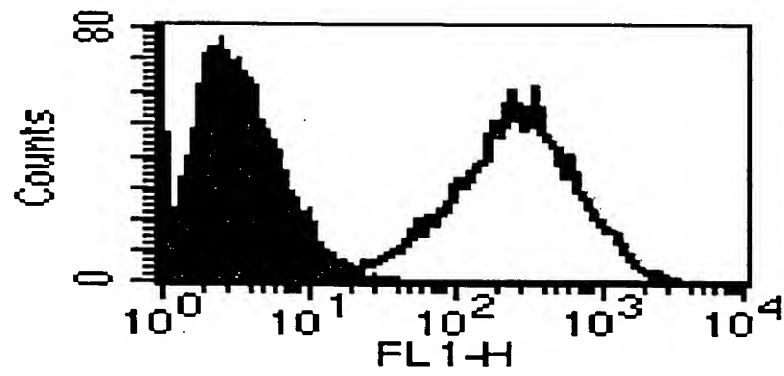


FIG. 1

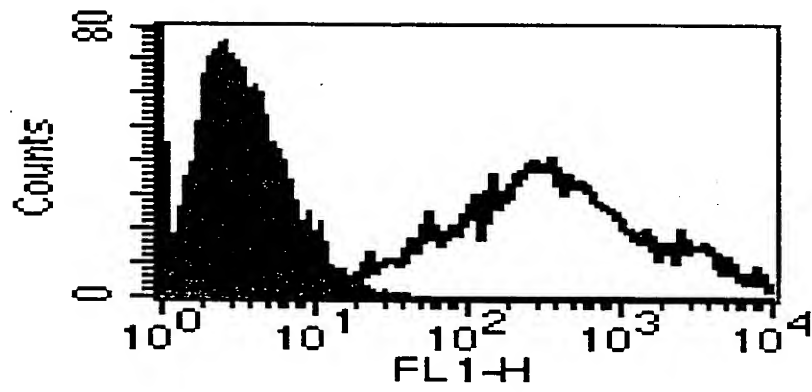


FIG. 2

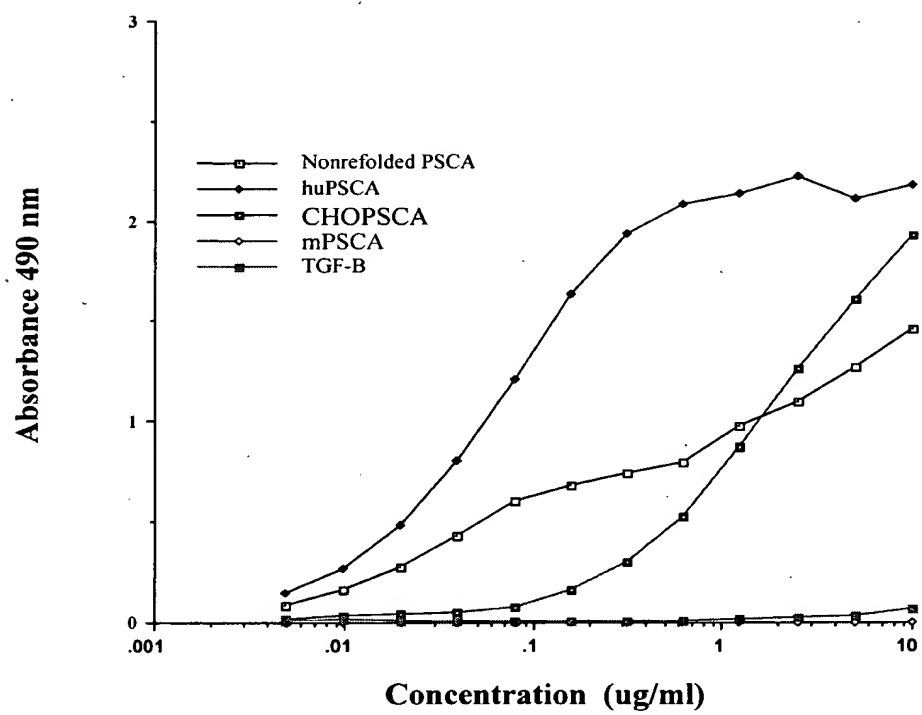


FIG. 3

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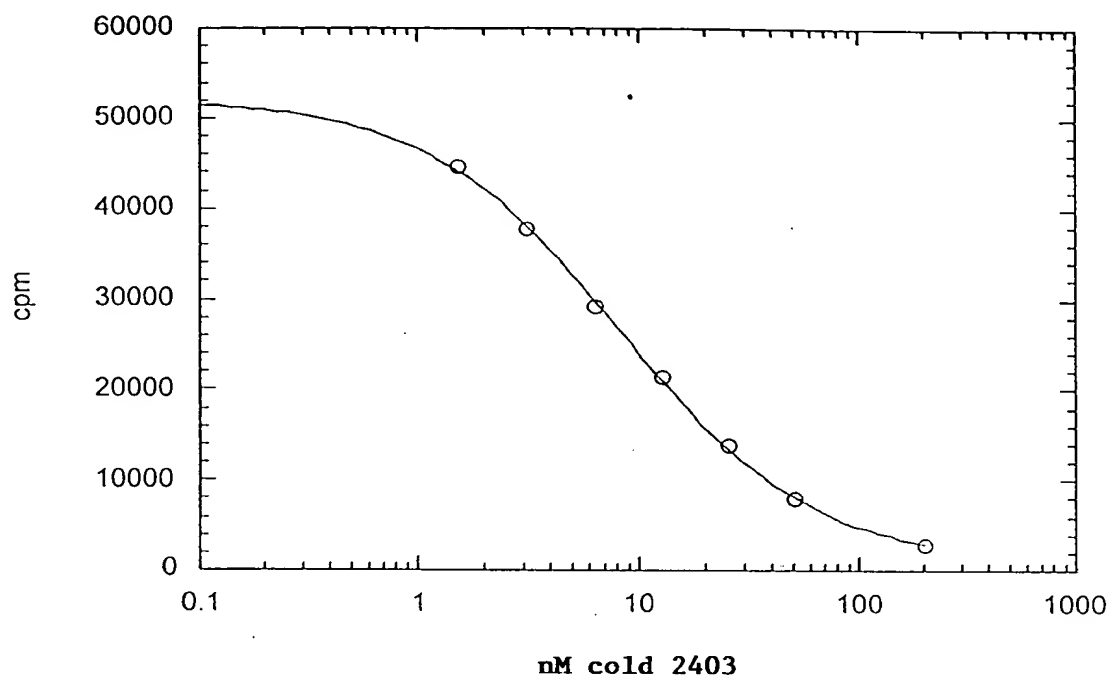


FIG. 4

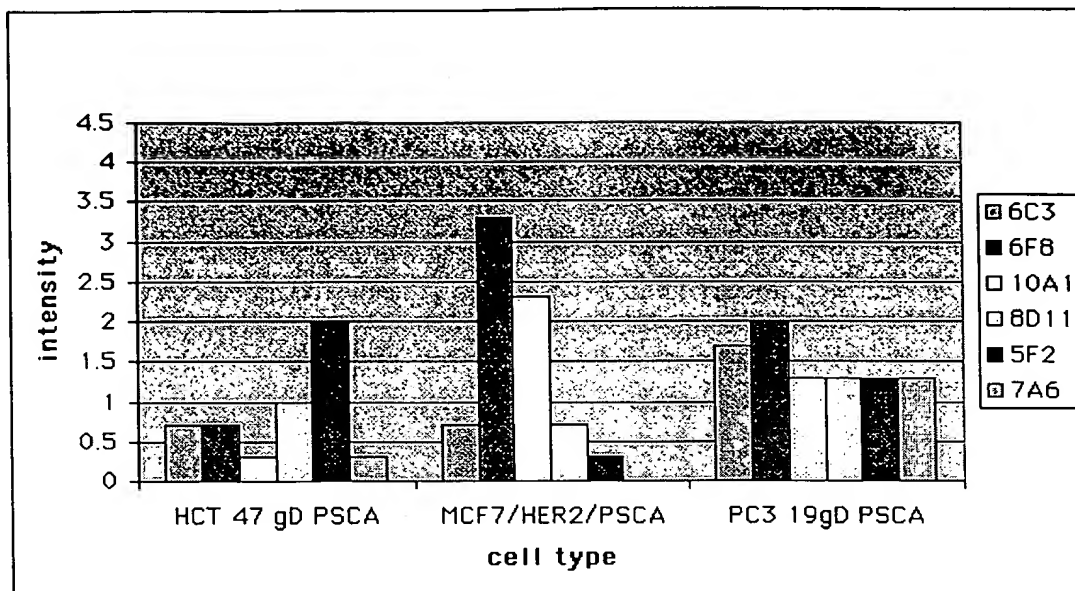


Fig. 5

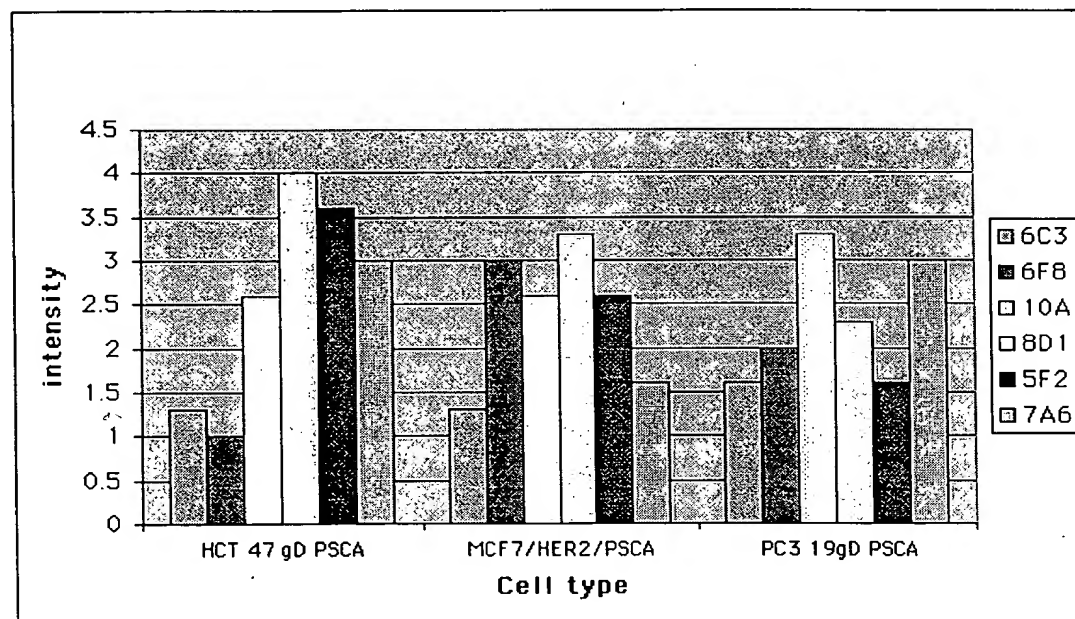


Fig. 6

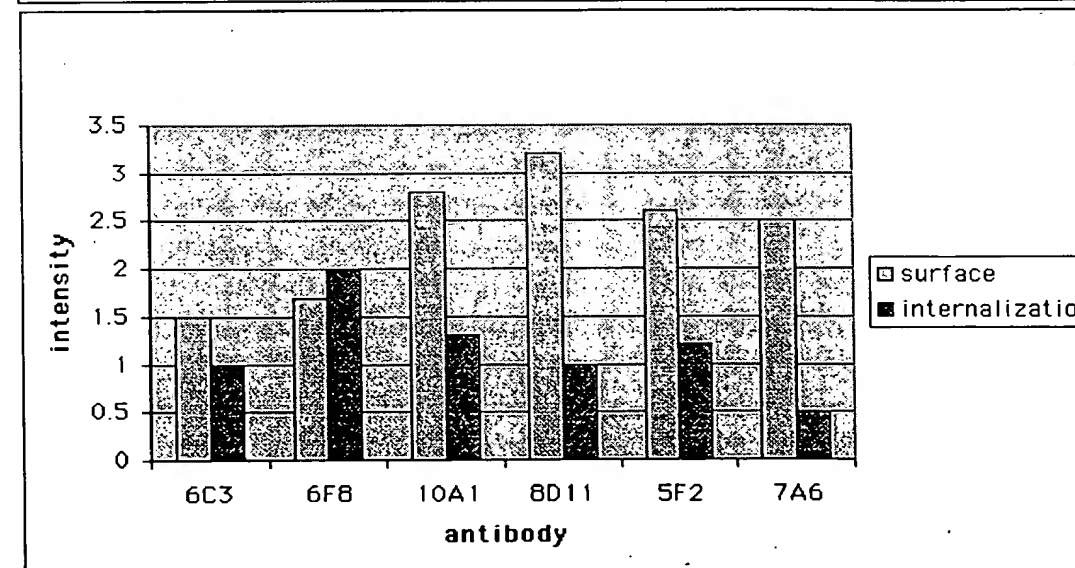


Fig. 7

FIG. 8A

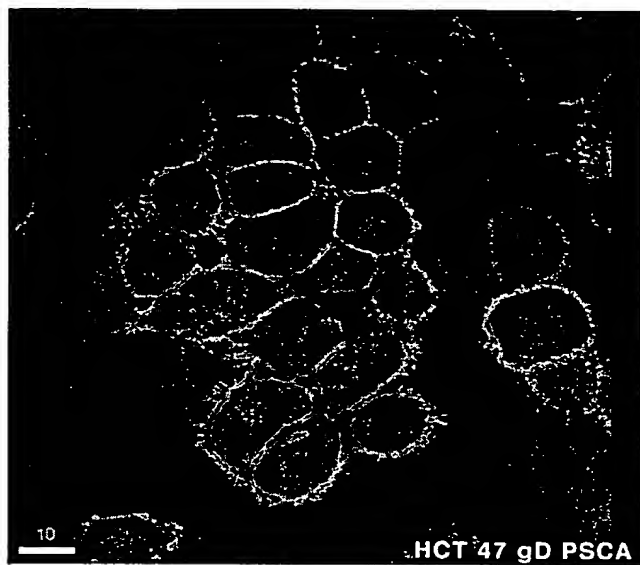


FIG. 8B

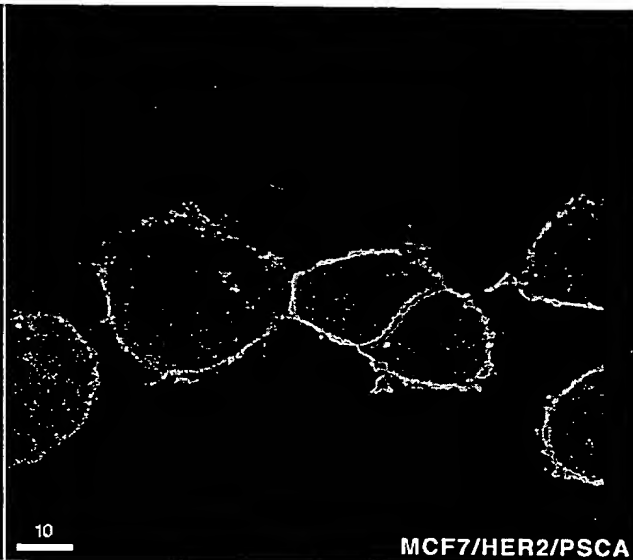


FIG. 8C

FIG. 9A

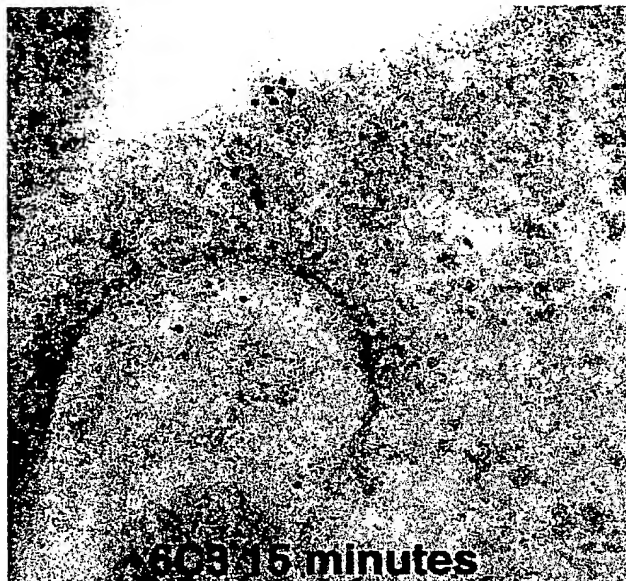


FIG. 9B

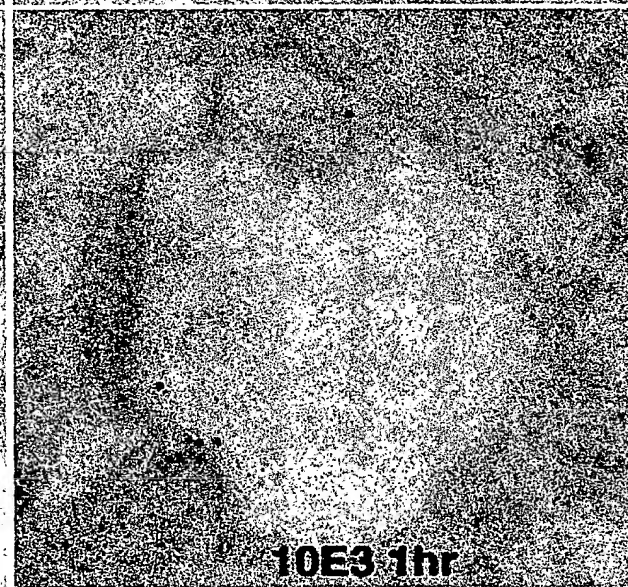
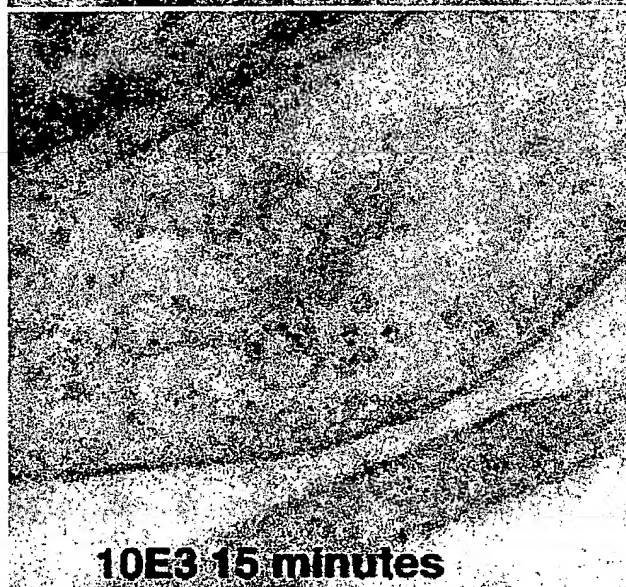
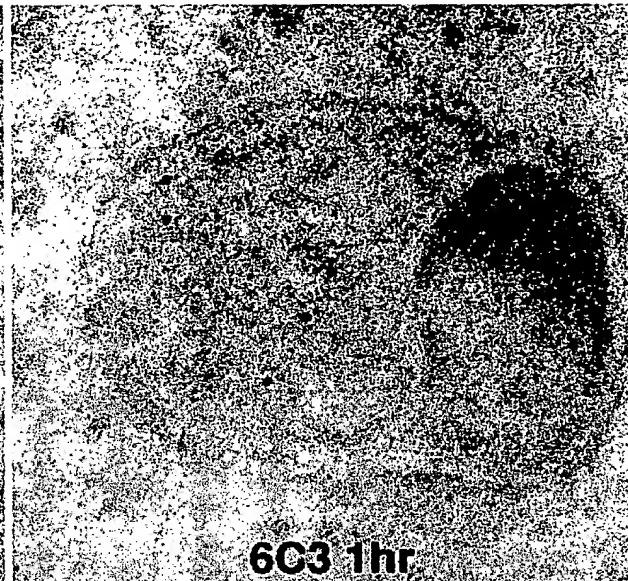


FIG. 9C

FIG. 9D

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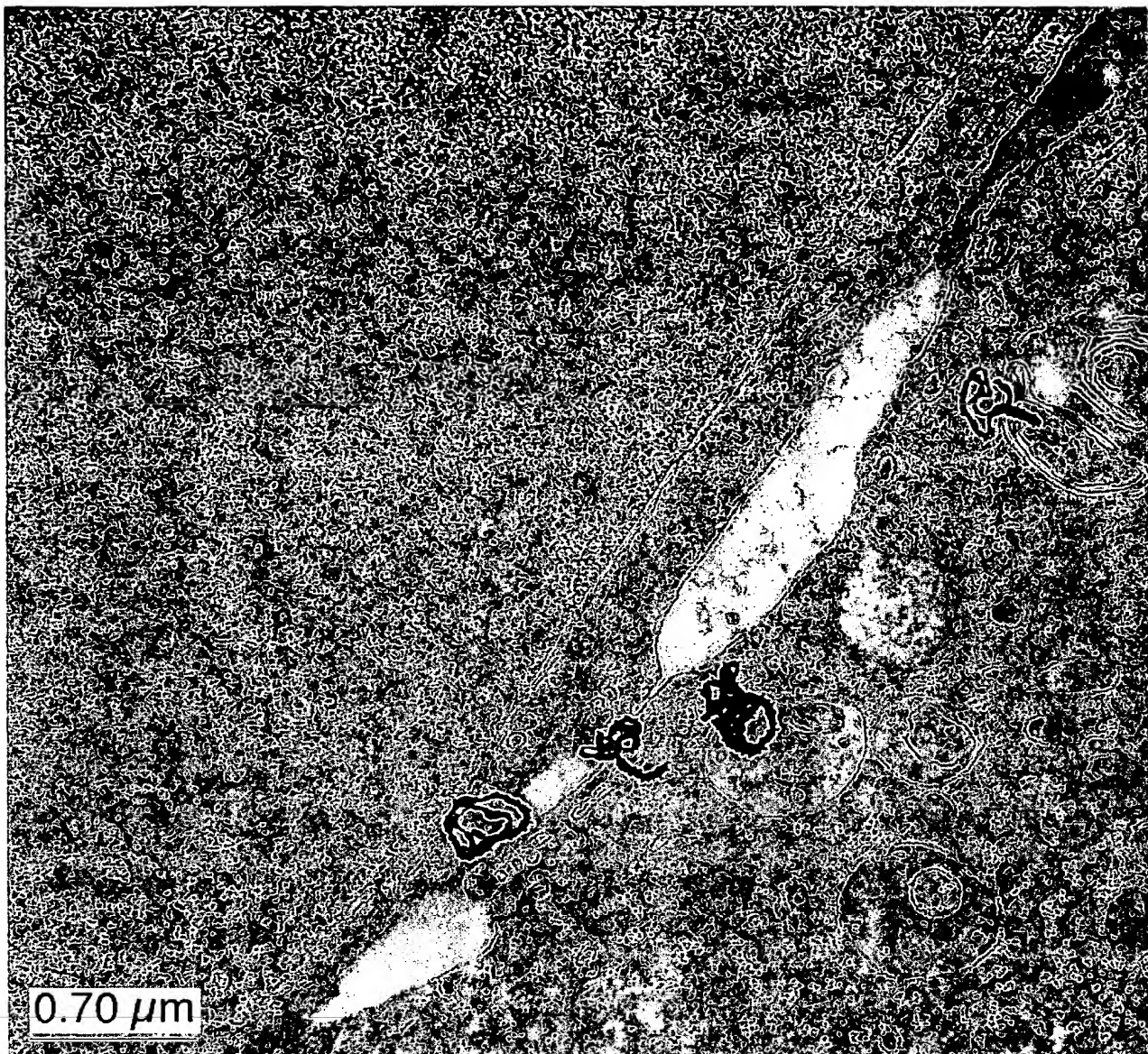


FIG. 10

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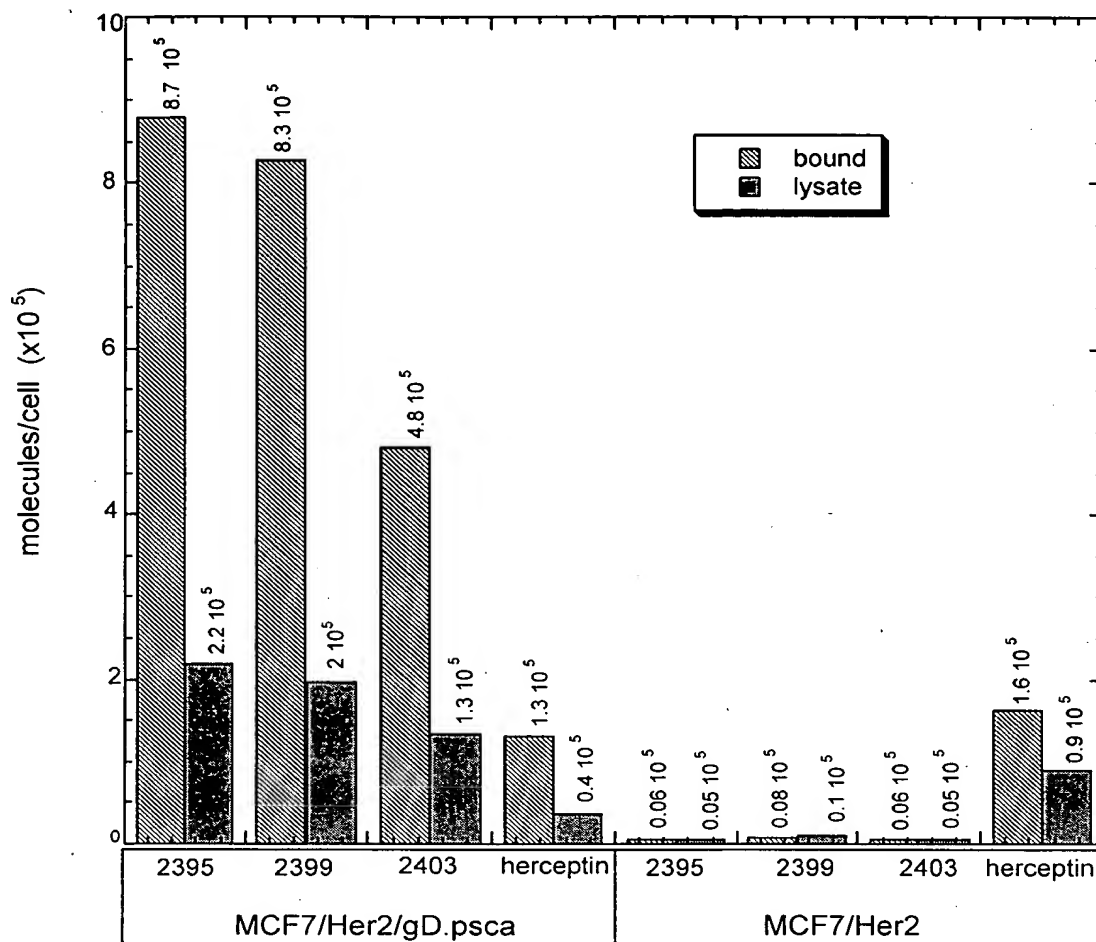


FIG. 11

Heavy chain sequences of anti-PSCA MAbs

	<u>CDR1</u>	<u>CDR2</u>
2395 :	N-----ELVKPGAPVKLSCKASGYTFTNYWMNWVKQRPGRGLEWIGRIDPSXXXQTFKDKA	
2399 :	N-----PGAELVKPGAPVKLSCKASGYTFTNYWMNWVKQRPGRGLEWIGRIDPSDSETQYNQTFKDKA	
2403 :	N-QVQVQQPGAELVKPGAPVKLSCKASGYTFTNYWLNWVKQRPGRGLEWIGRIDPSDSEIHYDQKFKDKA	
2761 :	N-EVQLQQSGPDLEKPGASVKISKPSGNSFTGYIHHWVKQSHGKSLEWIGRVDPNNGFTSYNQKFKGKA	
	<u>CDR3</u>	
2395 :	TLTVDKSSSTAYIQLSSLTSEDSAVYYCAITAAIAMDYWGQTSVTVSSAKTTGPS-C	
2399 :	TLTVDKSSSTAYIQLSSLTSEDSAVYYCAITAAIAMDYWGQTSVTVSSAKTTGPS-C	
2403 :	TLTVDKSSSTAYIQLSSLTSEDSAVYYCALTGIYAMAYWGQTSVTVSSAKTTGPS-C	
2761 :	ILTVDKSSSTAYMELRSLTSEDSAVYYCVG-NEFDS--WGQGTTLTVSSAKTTGPS-C	

Light chain sequences of anti-PSCA MAbs

	<u>CDR1</u>	<u>CDR2</u>
2395 :	N-----SVSISCRSSKSLHNSNGNTLYWFQRPQSPQLLIYRMSNLASGVDPDRFS	
2403 :	N-DIVMTQAAPSPVPTGESVSISCRSSKSLHNSNGNTLYWFQRPQSPQLLIYRMSNLASGVDPDRFS	
2761 :	N-DVVMTQTPLTSLVTIGQPASISCKSSQSLDSDGKTYLNWLLQRPQSPKRLLIYLVSTLDSGVDPDRFT	
	<u>CDR3</u>	
2395 :	GS GSGTVFTLRISRVEAEDVGYYCYCMQHLESFFTFGSGGTKLEIKR-C	
2403 :	GS GSGTAFTLRISRVEAEDVGYYCYCIQHLEYPPYTFGGGTKLELKR-C	
2761 :	GS GSGTDFTLTKISRVEAEDLGYYCYCWQGTHTFPRTFGGGTKLEIKR-C	

FIG. 12

chimeric 2403 (5F2.4H4.1E3) Light Chain

signal peptide MGWSCILFLVATATGVHS

DIVMTQAAPSPVPTGESVSISCRSSKSLLSNGNTYLYWFLQRPQSPQLLIYRMSNLASGVDPDRFSGSGGTAFTLRISRVEAEDVG
VYYCLQHLEYPYTFGGGKLELK/RTVAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS
TYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

chimeric 2403 (5F2.4H4.1E3) IgG Heavy Chain

signal peptide MGWSCILFLVATATGVHS

QVQVQQPGAELVKPGAPVKLSCKASGYTFTNYYLNNWVKQRPGRGLEWIGRIDPSDSEIHVDQKFKDKATLTVDKSSSTA YIQLSSLT
SEDSAVYYCALTGIYAMAYWGQTSVTVSSAKTTG/PSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL
QSSGLYSLSVTVPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRTPEVTCVVV
DVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVQLHQLWLNQKCKVSNKALPAPIEKTISKAKGQPREPQVYVY
LPDSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVVFSCVMHEALHNHYT
QKLSLSLSPGK

chimeric 2761 (6B8.1D7.2B3) Fab - Light Chain

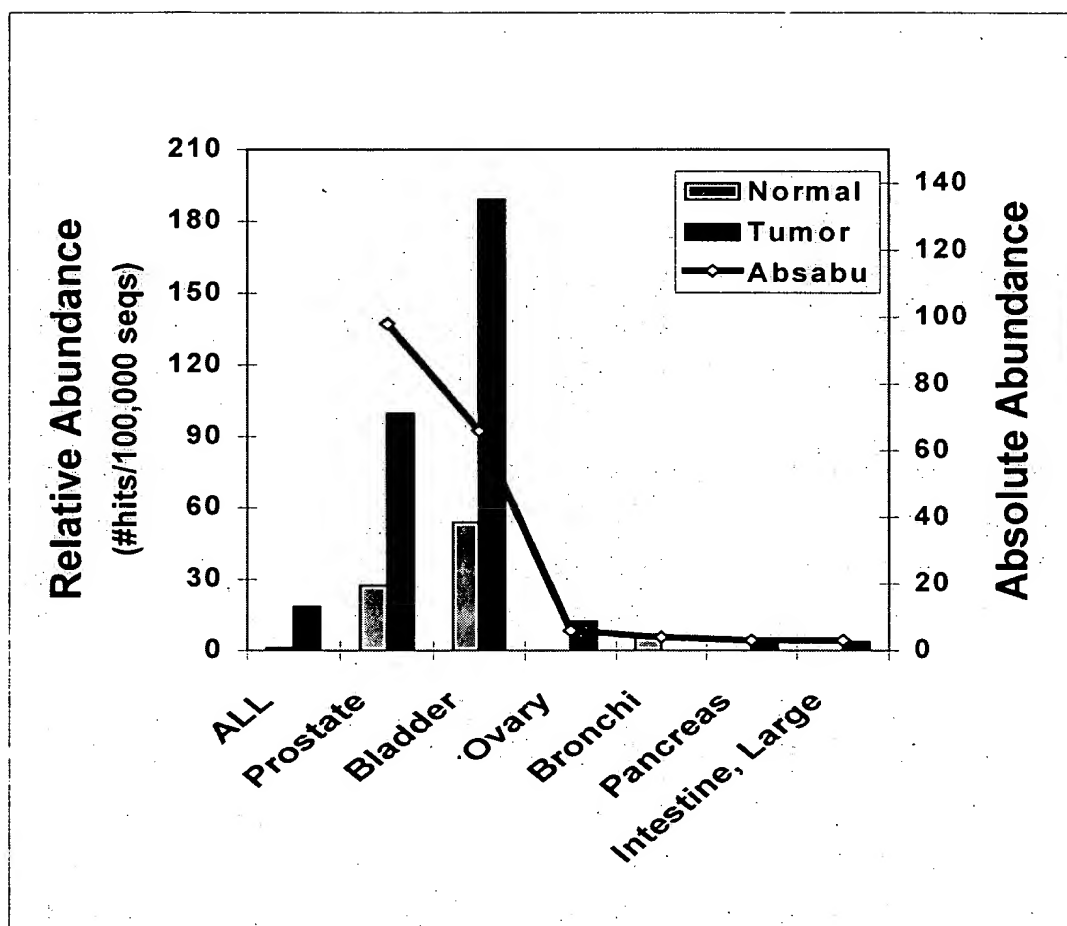
DVVMQTQPLTSLVTIGQPASISCKSSQSLLDSDGKTYLNNWLLQRPQGSPKRLIYLVSTLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGV
YYCWQGTHTFPRTFGGGKLEIKR [V_L/C_κ junction]
TVAAAPSVFIFPPSDEQLKSGTASVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACET
HQGLSSPVTKSFNRGEC

chimeric 2761 (6B8.1D7.2B3) Fab - Heavy chain

EVQLQQSGPDLEKPGASVKISCKPSGNSFTGYIHHWVKQSHGKSLEWIGRVDPNNGFTSYNQKFKGKAILTVDKSSSTA YMELRSLTSE
DSA VYYCVGNFFDSWGQGTTLTVSSA [V_H/C_γ1 junction]
KTTGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQTYICNVNHNKPSN
TKVDKKVEPKSCDKTHT

FIG. 13

FIG. 14



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1 ATGAAGGCTG TGCTGCTTGC CCTGTTGATG GCAGGCTTGG CCCTGCAGCC AGGCACTGCC
TACTTCCGAC ACGACGAACG GGACAACCTAC CGTCCGAACC GGGACGTCGG TCCGTGACGG
1 M K A V L L A L L M A G L A L Q P G T A

61 CTGCTGTGCT ACTCCTGCAA GGCCCAAGTG AGCAACGAGG ACTGCCTGAA TGTGGAGAAC
GACGACACGA TGAGGACGTT CCGGCTCCAC TCGTTGCTCC TGACGGACTT ACACCTCTTG
21 L L C Y S C K A Q V S N E D C L N V E N

121 TGCACGCAGC CGGAGGAGCA GTGCTGGACC GAGCGCATCC GCGCCGTGGG CCTCCTGACC
ACGTGCGTCG GCCTCCTCGT CACGACCTGG CTCGCGTAGG CGCGGCACCC GGAGGACTGG
41 C T Q P E E Q C W T E R I R A V G L L T

181 GTCATCAGCA AAGGCTGCAG CTCAAACTGC GTGGATGACT CACAGGACTA CTACGTGGGC
CAGTACTCGT TTCCGACGTC GAGTTTGACG CACCTACTGA GTGTCTGAT GATGCACCCG
61 V I S K G C S S N C V D D S Q D Y Y V G

241 AAGAAGAACA TCACCTGCTG TGACACCGAC TTGTGCAACG CCAGCGGGGC CCATGCACCTG
TTCTTCTTGT AGTGGACGAC ACTGTGGCTG AACACGTTGC GGTGCCCCCG GGTACGTGAC
81 K K N I T C C D T D L C N A S G A H A L

301 CAGCCGGCTG CTGCCATCCT GGCACCTGCTC CCTGCACTCA GTCTGCTGCT TTGGAGCCCC
GTCGCGCCGAC GACGGTAGGA CCGTGACGAG GGACGTGAGT CAGACGACGA AACCTCGGGG
101 Q P A A A I L A L L P A L S L L L W S P

361 AGACAGCTGT AG
TCTGTCGACA TC
121 R Q L O

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FIG. 15

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1 ATGAAGGCTG TGCTGCTTGC CCTGTTGATG GCAGGCTTGG CCCTGCAGCC AGGCACTGCC
TACTTCCGAC ACGACGAACG GGACAACCTAC CGTCCGAACC GGGACGTCGG TCCGTGACGG
1 M K A V L L A L L M A G L A L Q P G T A

61 CTGTTGTGCT ACTCCTGCAA GGCCCAAGTG AGCAACGAGG ACTGCCTGAA TGTGGAGAAC
GACAACACGA TGAGGACGTT CCGGCTCCAC TCGTTGCTCC TGACGGACTT ACACCTCTTG
21 L L C Y S C K A Q V S N E D C L N V E N

121 TGCACGCAGC CGGAGGAGCA GTGCTGGACC GAGCGCATCC GCGCCGTGGG CCTCCTGACC
ACGTGCGTCG GCCTCCTCGT CACGACCTGG CTCGCGTAGG CGCGGCACCC GGAGGACTGG
41 C T Q P E E Q C W T E R I R A V G L L T

181 GTCATCAGCA AAGGCTGCAG CTCAAACTGC GTGGATGACT CACAGGACTA CTACGTGGGC
CAGTACTCGT TTCCGACGTC GAGTTTGACG CACCTACTGA GTGTCTGAT GATGCACCCG
61 V I S K G C S S N C V D D S Q D Y Y V G

241 AAGAAGAACA TCACCTGCTG TGACACCGAC TTGTGCAACG CCAGCGGGGC CCATGCACCTG
TTCTTCTTGT AGTGGACGAC ACTGTGGCTG AACACGTTGC GGTGCCCCCG GGTACGGGAC
81 K K N I T C C D T D L C N A S G A H A L

301 CAGCCAGCTG CTGCCATCCT GGCACCTGCTC CCTGCACTCA GCCTGCTGCT TTGGGGCCCC
GTCGCTCGAC GACGGTAGGA CCGTGACGAG GGACGTGAGT CCGACGACGA AACCCCGGGG
101 Q P A A A I L A L L P A L S L L L W G P

361 AGACAGCTGT AG
TCTGTCGACA TC
121 R Q L O

```

FIG. 16

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	10	20	30	40	50
human	MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDECLQVENCTQLGEQCWT				

cynomolgus	MKAVLLALLMAGLALQPGTALLCYSCKAQVSNEDECLNVENCTQPEEQCWT				
	10	20	30	40	50
	60	70	80	90	100
human	ARIRAVGLLTVISKGCSLNCVDDSQDYVVGKKNITCCDIDLNASGAHAL				

cynomolgus	ERIRAVGLLTVISKGCSLNCVDDSQDYVVGKKNITCCDIDLNASGAHAL				
	60	70	80	90	100
	110	120			
human	QPAAAILALLPALGLLWGPGL				

cynomolgus	QPAAAILALLPALSLLLWSPRQL				
	110	120			

FIG. 17

004207" 50486960

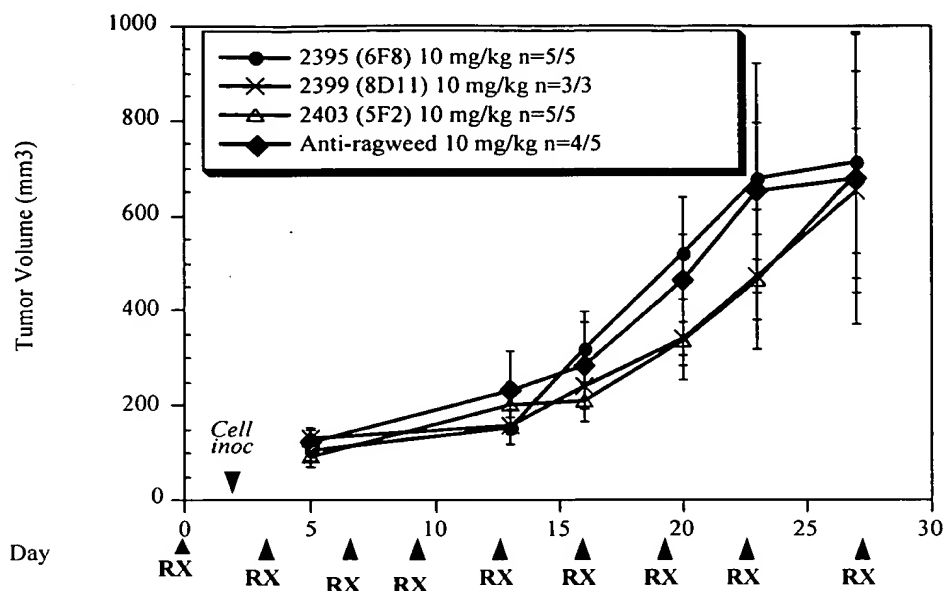


FIG. 18

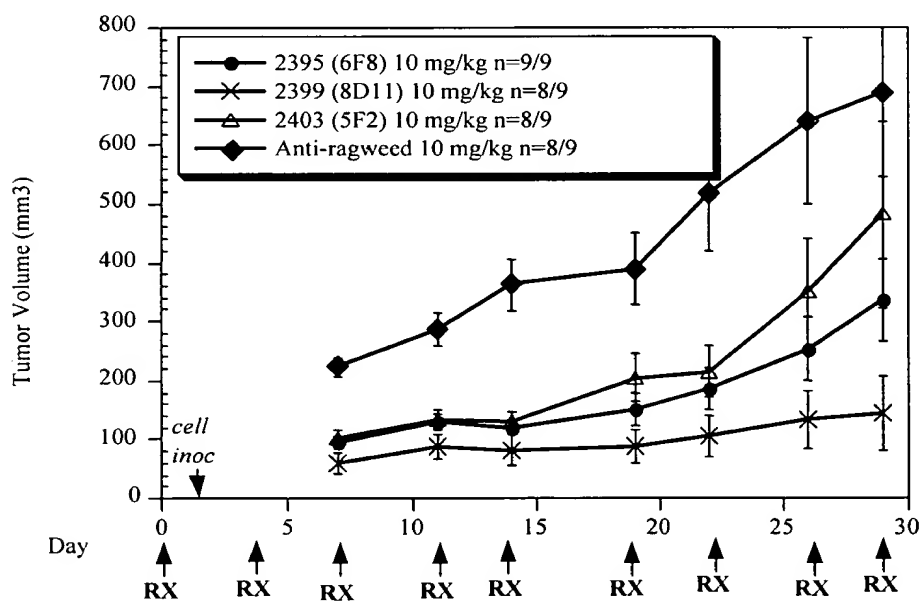


FIG. 19

002207" 50286960

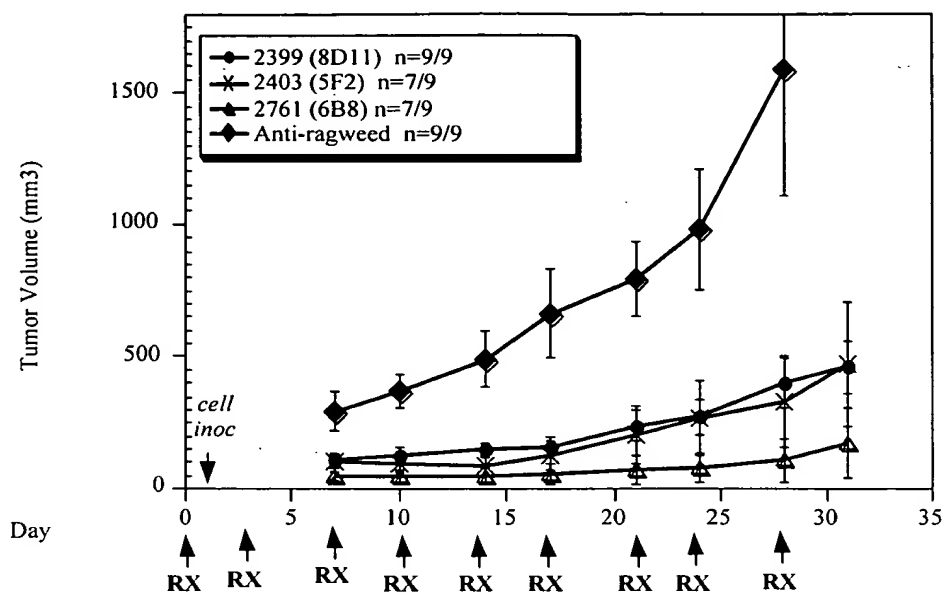


FIG. 20

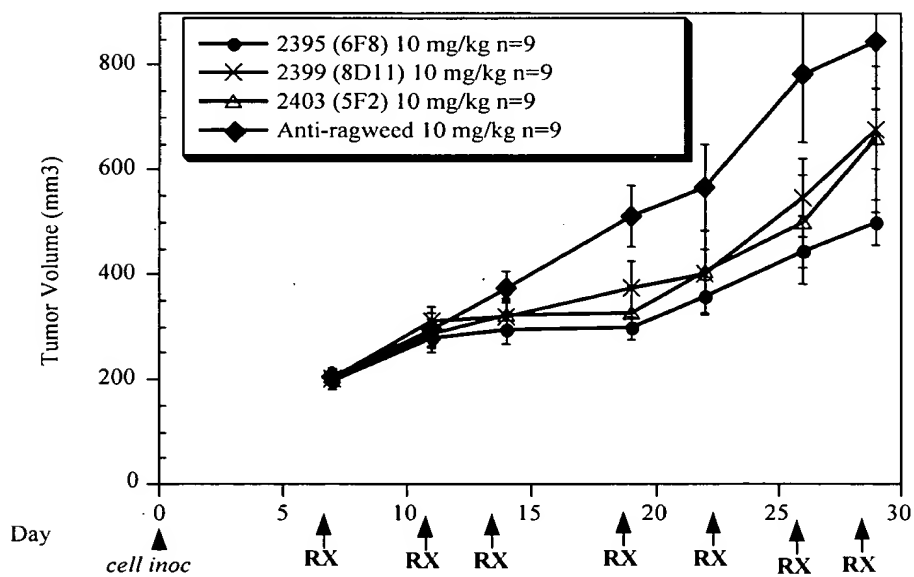


FIG. 21

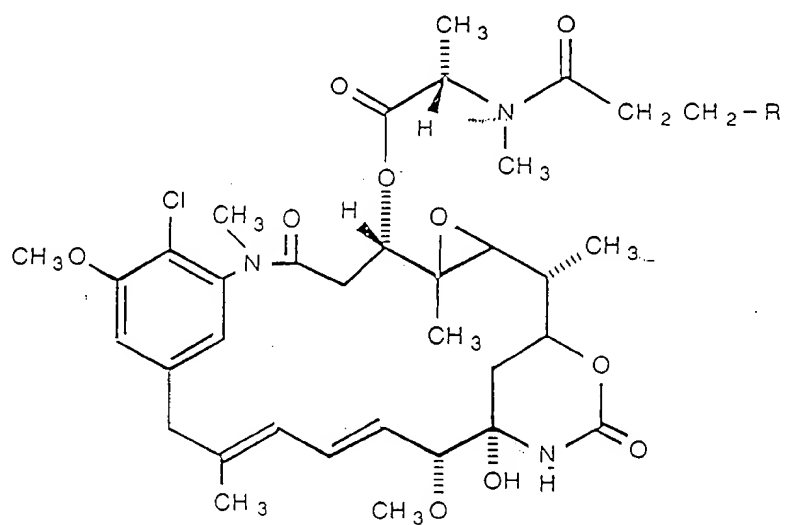


FIG. 22

002201" 50485950

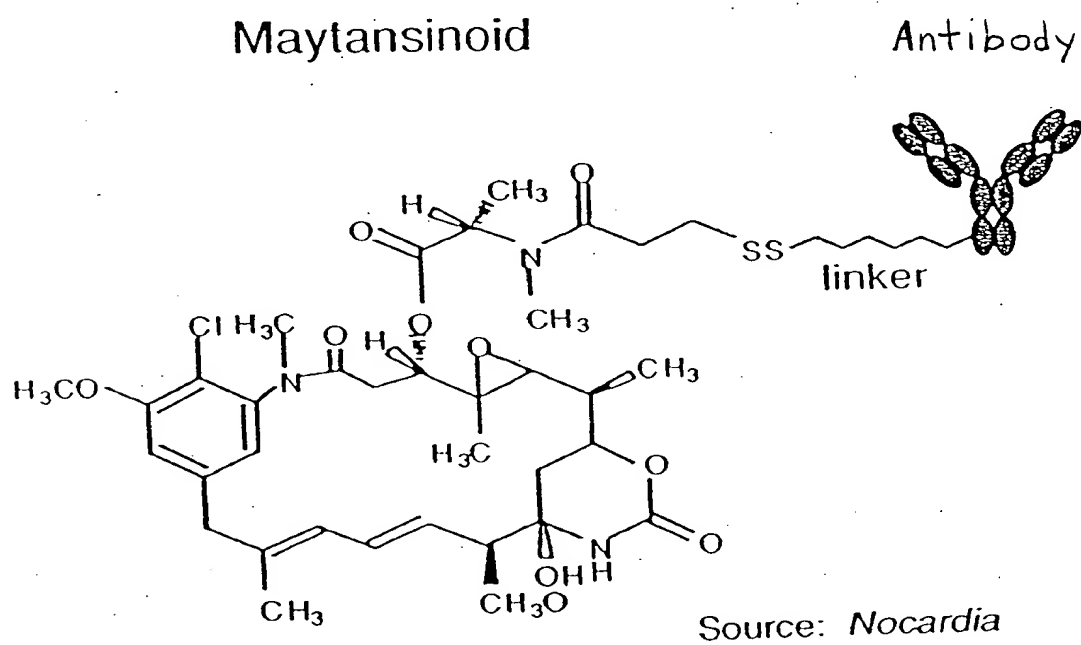


FIG. 23

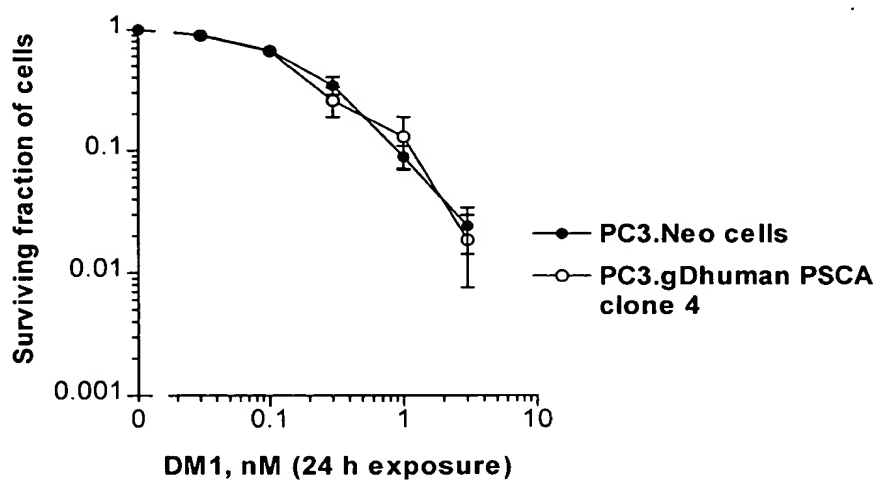


FIG. 24

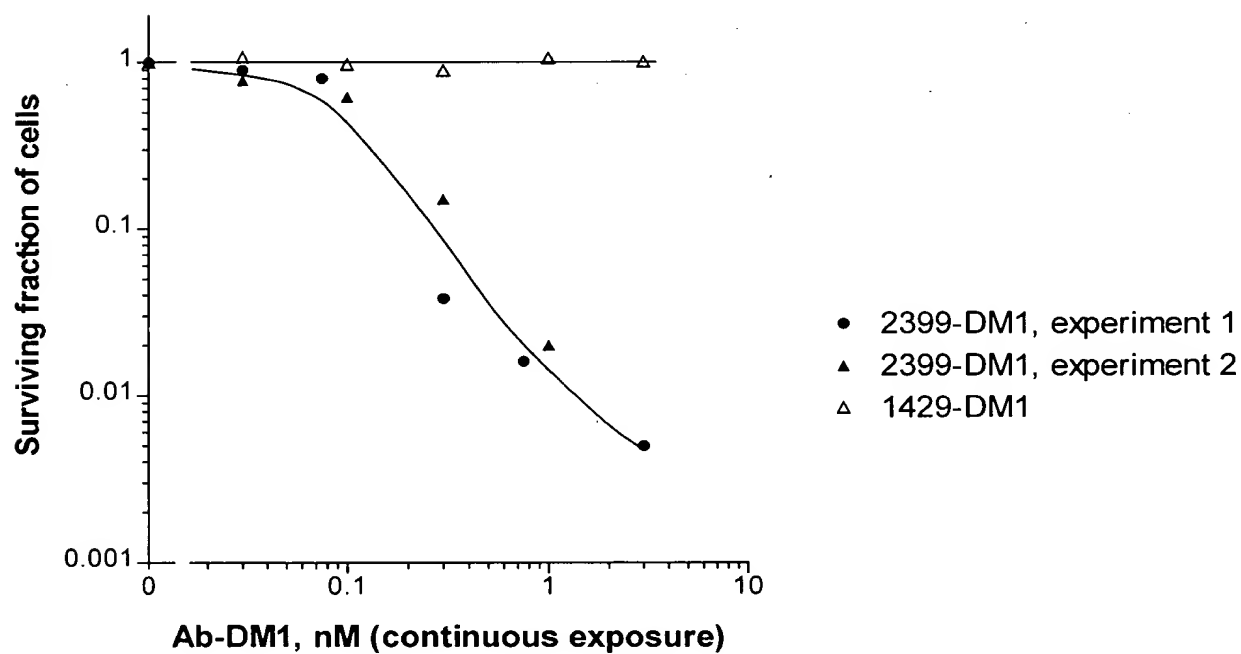


FIG. 25

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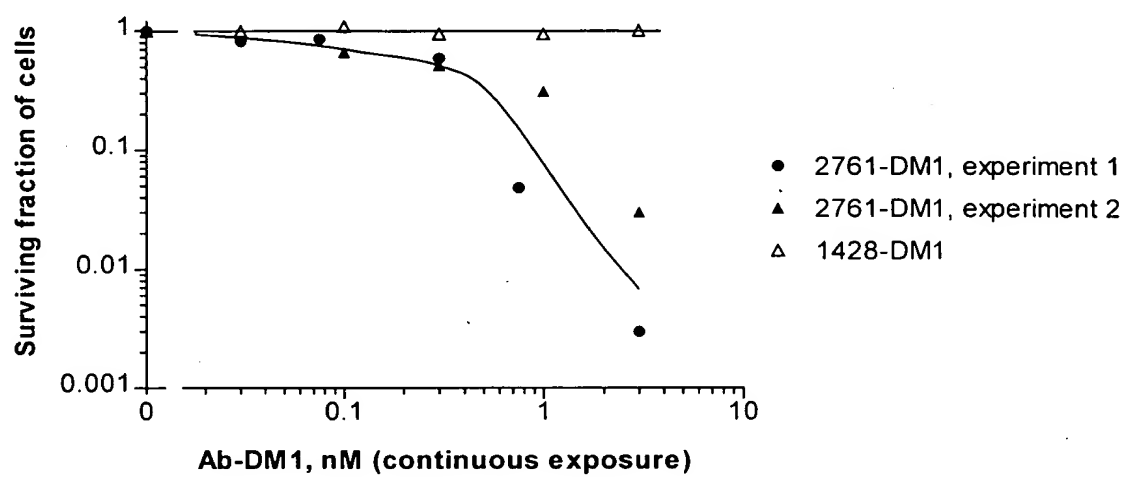


FIG. 26

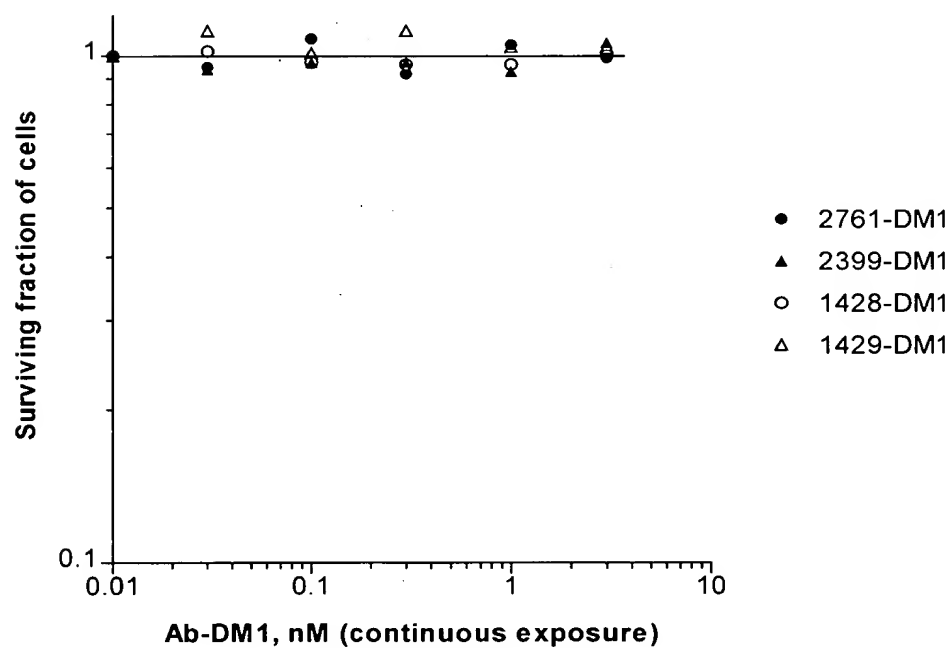


FIG. 27

FIG. 28

